

GEPHE SUMMARY

Zmr1 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~Zmr1^#gephebase-summary-title)	Gephebase Gene	GP00001715	GepheID
	Entry Status	Courtier	Main curator
	Published		

PHENOTYPIC CHANGE

Trait #1	Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Physiology^#gephebase-summary-title)	Trait
Xenobiotic resistance (fungicide) (https://www.gephebase.org/search-criteria?/and+Trait=~Xenobiotic resistance (fungicide)^#gephebase-summary-title)	Trait State in Taxon A
high melanin levels - lower growth rate in absence of fungicide - higher growth rate in presence of fungicide	Trait State in Taxon B
low melanin levels - higher growth rate in absence of fungicide	

Trait #2	Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Physiology^#gephebase-summary-title)	Trait
Melanin content (https://www.gephebase.org/search-criteria?/and+Trait=~Melanin content^#gephebase-summary-title)	Trait State in Taxon A
high melanin levels - lower growth rate in absence of fungicide - higher growth rate in presence of fungicide	Trait State in Taxon B
low melanin levels - higher growth rate in absence of fungicide	

Data not curated		Ancestral State	
Intraspecific (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Intraspecific^#gephebase-summary-title)		Taxonomic Status	
Taxon A	Latin Name	Taxon B	Latin Name
Zymoseptoria tritici (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Zymoseptoria tritici^#gephebase-summary-title)	Zymoseptoria tritici (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Zymoseptoria tritici^#gephebase-summary-title)		
-	Common Name	-	Common Name
	Synonyms		Synonyms
Zymoseptoria tritici (Desm.) Quaedvlieg & Crous 2011; CBS 115943; CBS:115943; IPO 323; IPO:323	Zymoseptoria tritici (Desm.) Quaedvlieg & Crous 2011; CBS 115943; CBS:115943; IPO 323; IPO:323		
species	Rank	species	Rank
	Lineage		Lineage
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Pezizomycotina; leotiomyceta; dothideomyceta; Dothideomycetes; Dothideomycetidae; Capnodiales; Mycosphaerellaceae; Zymoseptoria	cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Pezizomycotina; leotiomyceta; dothideomyceta; Dothideomycetes; Dothideomycetidae; Capnodiales; Mycosphaerellaceae; Zymoseptoria		
	Parent		Parent
Zymoseptoria () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1047167)	Zymoseptoria () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1047167)		
1047171 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1047171)	1047171 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1047171)		
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
Yes		Yes	
	Taxon A Description		Taxon B Description
strain 3D7		strain 3D1	

GENOTYPIC CHANGE

CMR1	Generic Gene Name	UniProtKB Cochliobolus heterostrophus
		Q06F33 (http://www.uniprot.org/uniprot/Q06F33)
	Synonyms	GenebankID or UniProtKB
	String	0
-		
-		
-	Sequence Similarities	
GO - Molecular Function		
GO:0008270 : zinc ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0008270)		
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)		
GO:0000981 : DNA-binding transcription factor activity, RNA polymerase II-specific (https://www.ebi.ac.uk/QuickGO/term/GO:0000981)		
GO - Biological Process		
GO:0006351 : transcription, DNA-templated (https://www.ebi.ac.uk/QuickGO/term/GO:0006351)		
GO - Cellular Component		
GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)		
Mutation #1		
No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)		Presumptive Null
Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Cis-regulatory^#gephebase-summary-title)		Molecular Type
Insertion (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Insertion^#gephebase-summary-title)		Aberration Type
10-100 kb		Insertion Size
Molecular Details of the Mutation		
insertion of a transposable element island (13 TE interspersed by simple repeats) of approximately 30 kb, located 1862 bp upstream of Zmr1 start codon - analysis of knock out lines of the TE island insertion		
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title)		Experimental Evidence
Transposable element insertions shape gene regulation and melanin production in a fungal pathogen of wheat. (2018) (https://pubmed.ncbi.nlm.nih.gov/30012138)		Main Reference
Krishnan P; Meile L; Plissonneau C; Ma X; Hartmann FE; Croll D; McDonald BA; SÄınchez-Vallet A		Authors
Abstract		
Fungal plant pathogens pose major threats to crop yield and sustainable food production if they are highly adapted to their host and the local environment. Variation in gene expression contributes to phenotypic diversity within fungal species and affects adaptation. However, very few cases of adaptive regulatory changes have been reported in fungi and the underlying mechanisms remain largely unexplored. Fungal pathogen genomes are highly plastic and harbor numerous insertions of transposable elements, which can potentially contribute to gene expression regulation. In this work, we elucidated how transposable elements contribute to variation in melanin accumulation, a quantitative trait in fungi that affects survival under stressful conditions.		
We demonstrated that differential transcriptional regulation of the gene encoding the transcription factor Zmr1, which controls expression of the genes in the melanin biosynthetic gene cluster, is responsible for variation in melanin accumulation in the fungal plant pathogen Zymoseptoria tritici. We show that differences in melanin levels between two strains of Z. tritici are due to two levels of transcriptional regulation: (1) variation in the promoter sequence of Zmr1 and (2) an insertion of transposable elements upstream of the Zmr1 promoter. Remarkably, independent insertions of transposable elements upstream of Zmr1 occurred in 9% of Z. tritici strains from around the world and negatively regulated Zmr1 expression, contributing to variation in melanin accumulation.		
Our studies identified two levels of transcriptional control that regulate the synthesis of melanin. We propose that these regulatory mechanisms evolved to balance the fitness costs associated with melanin production against its positive contribution to survival in stressful environments.		
		Additional References

Mutation #2	
No (https://www.gephebase.org/search-criteria?/and+Presumptive Null="No"#gephebase-summary-title)	Presumptive Null
Cis-regulatory (<a cis-regulatory"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Molecular Type=">https://www.gephebase.org/search-criteria?/and+Molecular Type="Cis-regulatory"#gephebase-summary-title)	Molecular Type
SNP (https://www.gephebase.org/search-criteria?/and+Aberration Type="SNP"#gephebase-summary-title)	Aberration Type
several candidate SNP - tests using reporter transgenes	Molecular Details of the Mutation
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence="Linkage Mapping"#gephebase-summary-title)	Experimental Evidence
Transposable element insertions shape gene regulation and melanin production in a fungal pathogen of wheat. (2018) (https://pubmed.ncbi.nlm.nih.gov/30012138)	Main Reference
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stressful conditions.

We demonstrated that differential transcriptional regulation of the gene encoding the transcription factor Zmr1, which controls expression of the genes in the melanin biosynthetic gene cluster, is responsible for variation in melanin accumulation in the fungal plant pathogen *Zymoseptoria tritici*. We show that differences in melanin levels between two strains of *Z. tritici* are due to two levels of transcriptional regulation: (1) variation in the promoter sequence of Zmr1 and (2) an insertion of transposable elements upstream of the Zmr1 promoter. Remarkably, independent insertions of transposable elements upstream of Zmr1 occurred in 9% of *Z. tritici* strains from around the world and negatively regulated Zmr1 expression, contributing to variation in melanin accumulation.

Our studies identified two levels of transcriptional control that regulate the synthesis of melanin. We propose that these regulatory mechanisms evolved to balance the fitness costs associated with melanin production against its positive contribution to survival in stressful environments.

Additional References

RELATED GEPHE

	Related Genes
No matches found.	
	Related Haplotypes
No matches found.	

EXTERNAL LINKS

COMMENTS

@TE ; check for UniProtKB and orthology with Cmr1